

Supplementary Material

Changes of cadmium storage forms and isotope ratios in rice during grain filling

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Tables

Table S 1: Quality assessment	2
Table S 2: Dry weight and micro nutrients root and shoot	2
Table S 3: Cadmium concentration, mass balance, Cd isotopes	3
Table S 4: Soil chemical parameters at flowering and maturity	3
Table S 5: Dry weight, Cd concentration, Cd mass, Cd isotopes in the upper shoot at maturity	4
Table S 6: Results of linear combination fits of XANES and EXAFS spectra for the soils and plant parts	5
Table S 7: Dry weight and micronutrient concentrations in the upper shoot at maturity.	6

Figures

	1 1	\sim
Figure S I. Overview rice part	s analyzed	n
inguic_0 if Overview file pure	⁵ unury 2Cu	9

1 Tables

Table_S 1: Quality assessment

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sample type	description	element	refere concenti	nce ration	measu concentr	red ationª		recovery digestion ^b
			[mg (kg weight	dry) ⁻¹]	[mg (kg weight	dry) ⁻¹]		% ^b
			mean	±sd ^d	mean	±sd ^d	nď	mean
rice shoot ^h	internal ISTerre rice standard		-	-	24.6	1.19	9	-
white cabbage	BCR-679	Cd ^a	1.66	0.07	1.77	0.05	3	107
soil	NIST SRM 2711		41.7	-	38.2	0.32	2	92
rice shoot ^h	internal ISTerre rice standard		-	-	35.9	1.84	9	-
white cabbage	BCR-679	Zn	79.70		92.36	2.06	3	116
soil	NIST SRM 2711		350		345	6.00	2	98
rice shoot ^h	internal ISTerre rice standard		-	-	6.48	0.46	8	-
white cabbage	BCR-679	Cu	2.89		2.93	0.20	3	101
soil	NIST SRM 2711		114		104	2.01	2	91
rice shoot ^h	internal ISTerre rice standard		-	-	1.41	0.06	8	-
white cabbage	BCR-679	Ni	27.0		30.34	1.73	3	113
soil	NIST SRM 2711		20.6		18.2	0.23	2	88
rice shoot ^h	internal ISTerre rice standard		-	-	232	9.05	8	-
white cabbage	BCR-679	Mn	13.3		15.52	0.34	3	117
soil	NIST SRM 2711		638		659	14.7	2	103

^adata from Wiggenhauser et al. 2020 ^bequal to [measured concentration] / [reference concentration] *100 ^cnumber of processing replicates (individually digested, purified for isotope analysis, and measured) ^dsd = standard deviation of the mean

Table_S 2: Dry weight and micro nutrients root and shoot

		1	DW		:	Zn			N	Mn			I	Ni			c	u	
compartment	period/growth stage	dry	weight	conce	ntration	n	nass	conce	entration	n	nass	conce	entration	n	nass	conce	entration	п	lass
			g	Ч	g g ⁻¹		нà	μ	g g ^{.1}		µg	μ	g g ⁻¹		hà	μ	g g ⁻¹		нà
		mean	±sda	mean	±sda	mean	±sda	mean	±sda	mean	±sdª	mean	±sda	mean	±sda	mean	±sda	mean	±sda
	flowering	25.3	0.66 B	43.5	6.97 A	1101	186 A	209	21.1 A	5284	620 B	2.57	0.81 A	64.9	20.2 A	10.9	1.85 A	277	50.2 A
whole plant	maturity	45.0	3.22 A	44.1	2.89 A	1979	88.4 A	206	11.2 A	9291	1158 A	1.90	0.20 A	85.7	12.8 A	6.93	0.64 B	311	22.0 A
	grain filling ^b	19.69	3.29	0.62	7.55	878	206	-2.56	23.9	4007	1314	-0.67	0.8	20.7	23.9	-4.01	2.0	33.6	54.9
	flowering	4.55	0.70 b	76.1	9.31 a	351	92.5 a	87.5	25.2 a	407	165 a	10.1	2.61 a	47.3	18.1 a	35.1	3.43 a	161	38.1 a
root	maturity	6.55	2.08 a	67.8	7.92 a	433	81.8 a	88.8	18.4 a	606	328 a	8.16	2.21 a	52.2	15.1 a	24.8	3.89 b	157	28.0 a
	grain filling⁵	2.00	2.2	-8.26	12.2	81.7	123	1.33	31.2	199	367	-1.99	3.42	4.85	23.6	-10.36	5.19	-4.09	47.3
	flowering	20.8	0.74 b	36.2	5.26 a	750	97.0 b	235	27.3 a	4876	549 b	0.85	0.13 a	17.6	2.27 b	5.59	0.67 a	116	12.9 a
shoot	maturity	38.4	1.48 a	40.3	3.42 a	1546	106 a	226	16.1 a	8685	836 a	0.87	0.15 a	33.5	6.64 a	4.01	0.59 b	154	20.0 a
	grain filling ^b	17.7	1.66	4.04	6.27	796	143	-9.46	31.7	3809	1000	0.02	0.20	15.9	7.02	-1.58	0.89	37.7	23.7
	flowering	NA	NA	378	103	NA	NA	519	26.8	NA	NA	1.65	0.32	NA	NA	13.17	2.74	NA	NA
nodes	maturity	NA	NA	813	315	NA	NA	428	37.3	NA	NA	1.51	0.10			18.81	0.90	NA	NA
	grain filling⁵	NA	NA	435	166	NA	NA	-91	23	NA	NA	-0.14	0.17	NA	NA	5.64	1.44	NA	NA
grain	harvest	4.83	1.01	26.9	1.24	130	25.6	26.1	5.3	125	29.9	1.60	0.35	7.75	2.35	4.78	0.69	23.01	5.70
*sd = standard deviation o sum test. e calculation as	f the mean of n = 4 experi desscribed in equation 4-8	mental replica 5.	ites, except for the	nodes (pooled	to n = 2 replicat	es (error bar = 2:	sd) to obtain suffic	ient material for	all analysis). Lett	ers indicate sigr	ificant difference:	s of the mean (up	per case = whole	plant, lower case	e italic = root, lowe	r case regular =	shoot) determined	Welch/s t-test	or Wilcoxon rank

compartment	period/growth stage	Cd con	centrat	ion	Cd	mass		Cd is	sotopes	
		hi	g g ⁻¹		I	ndc		δ ^{114/11}	¹⁰ Cd [‰]]
		mean	±sda		mean	±sda		mean	±sda	
	flowering	151	24.9	А	3828	709	Α	-0.45	0.01	А
whole plant	maturity	75.0	11.0	В	3380	590	А	-0.39	0.05	А
	grain filling⁵	-75.90	27.3	-	-448	922		0.06	0.05	_
	flowering	706	74.6	а	3214	628	а	-0.47	0.01	а
root	maturity	420	66.5	b	2679	543	а	-0.45	0.07	а
	grain filling ^b	-285	99.9	-	-536	831		0.03	0.07	-
	flowering	29.6	4.61	а	614	91.6	а	-0.31	0.03	b
shoot	maturity	18.3	2.43	b	701	84.6	а	-0.17	0.02	а
	grain filling ^b	-11.3	5.21	-	87.5	125		0.14	0.04	-
	flowering	21.2	0.30	NA	NA	NA	NA	0.33	0.00	NA
nodes	maturity	54.0	18.0	NA	NA	NA	NA	0.52	0.12	NA
	grain filling ^b	32.9	9.03	-	NA	NA		0.18	0.06	-
grain	harvest	0.98	0.05		4.73	1.03		0.49	0.01	

Table_S 3: Cadmium concentration, mass balance, Cd isotopes

^asd = standard deviation of the mean of n = 4 experimental replicates, except for the nodes (pooled to n = 2 replicates (error bar = 2sd) to obtain sufficient material for all analysis). Letters indicate significant differences of the mean (upper case = whole plant, lower case italic = root, lower case regular = shoot) determined using a Welch's t-test or Wilcoxon rank sum test (whole plant isotope ratios, Cd mass shoot). ^{*b}alance calculation as described in equations 4-5. ^cCd mass is given as µg (pot)², one pot contains 1.5kg and 22500 µg Cd

Table_S 4: Soil chemical	parameters at	flowering and	maturity

period/ growth stage	rhiz	on pH ^ь		rhizon Eh ^b			Ca(NO ₃) ₂ soil extractable Cd							
							[mg (kg soil) ⁻¹]			δ ^{114/110} Cd [‰]				
%	mean	±sd	n	mean	±sd	n	mean	±sd	n	mean	±2sd	n		
vegatative ^a	4.52	0.67	10 ^c	235	45.5	10 ^c								
grain filling	4.98	0.23	2 ^c	233	23.2	2 ^c								
flowering	5.52	0.24	3	195	22.3	3	3.52	2.10	2	-0.18	0.04	2		
maturity	5.14	0.11	4	217	5.1	4	3.65	0.23	2	-0.07	0.04	2		

^aData obtained in Wiggenhauser et al. (2020)

^bsoil pH determined using rhizon samplers (see methods) ^cn = sampling time points during the growth period

Table_S 5: Dry weight, Cd concentration, Cd mass, Cd isotopes in the upper shoot at maturity

compartment	dry	weight	conc	Cd centration	Cd	mass		Cd is	otope	S
		g	I	µg g⁻¹		μg ^ь		$\delta^{114/11}$	°Cd [%	60]
	mean	±sdª	mean	±sd ^a	mean	$\pm sd^{a}$		mean	±sdª	
shoot straw	38.4 25.6	1.48 0.96	18.3 25.5	2.43 3.02	701 676	84.6 84.3	_	-0.17 -0.20	0.02 0.02	_
flag leaves	1.51	1.14 b	1.35	0.25 b	1.88	1.17	с	-0.01	0.05	с
panicle	2.81	0.69 a	6.52	1.24 a	18.3	6.03	а	0.41	0.04	b
grains	4.83	1.01 c	0.98	0.05 c	4.73	1.03	b	0.49	0.01	а
average/sum	9.14	1.68	2.95	3.10	24.9	6.23	_	0.39	0.03	-

^asd = standard deviation of the mean of n = 4 experimental replicates. For the grain filling balance calculations (italic), the sd was calculated using error propagation as described in equation 4-5. Letters indicate significant differences of the mean determined using ANOVA for Cd mass fraction
^bCd mass is given as µg (pot)⁻¹, one pot contains 1.5kg and 22500 µg Cd

Table_	_S 6:	Results of	of linear	combinatio	n fits of	XANES	and	EXAFS	spectra	for the	soils	and p	olant
parts													

Sample ID + fit	Percentages	of Cd spe	cies	Percentages normalized to 100%					
Compartment	Sample name	fit in	fitting range (in eV or Å-1)	Cd-thiol or mixed/ amorph. CdSª	Cd-O	sum	Cd-thiol or mixed/ amorph. CdS	Cd-O	R factor ^b
grain	grain_Mat_I	XANES	-20 to 80	85	16	100	84	16	1.70E-02
straw	straw_Mat-III	XANES	-20 to 80	21	78	99	21	79	6.50E-03
	straw_Mat-II	XANES	-20 to 80	21	79	100	21	/9	4.88E-03
	straw_Mat-I	XANES	-20 to 80	19	83	103	19	81	6.04E-03
shoot	shoot_Flow_I	XANES	-20 to 80	75	25	100	75	25	1.20E-03
		EXAFS	3 to 12	68	33	100	68	33	1.33E-01
node	node_Mat_II	XANES	-20 to 80	100	0	100	100	0	2.86E-03
		EXAFS	3 to 11	109	0	109	100	0	2.57E-01
	node_Mat_I	XANES	-20 to 80	100	0	100	100	0	1.64E-03
		EXAFS	3 to 10.5	103	0	103	100	0	5.54E-02
	node Flow I	XANES	-20 to 80	100	0	100	100	0	8.40E-04
		EXAFS	3 to 11	106	0	106	100	0	1.38E-01
	node_Flow_II	XANES	-20 to 80	100	0	100	100	0	2.04E-03
root	root_Mat_I	XANES	-20 to 80	100	0	100	100	0	7.49E-03
		EXAFS	3 to 11	109	0	109	100	0	3.52E-02
	root_Mat_Ia	XANES	-20 to 80	100	0	100	100	0	2.83E-03
		EXAFS	3 toll	101	0	101	100	0	5.80E-02
	root_Mat_II	XANES	-20 to 80	100	0	100	100	0	1.72E-03
		EXAFS	3 to11.7	93	6	99	94	6	4.11E-02
	root_Flow_I	XANES	-20 to 80	100	0	100	100	0	1.13E-03
		EXAFS	3 to10.7	107	0	107	100	0	3.84E-02
soil	soil_Mat_II	XANES	-20 to 80	75	25	100	75	25	1.04E-03
	soil_Mat_I	XANES	-20 to 80	53	47	100	53	47	3.40E-03
	soil_Flow_I	XANES	-20 to 80	38	63	101	38	62	1.90E-03
		EXAFS	3 to 11	34	65	99	34	66	1.27E-01
	soil_Flow_Ia	XANES	-20 to 80	11	88	99	11	89	1.80E-03
	soil_Flow_II	XANES	-20 to 80	31	69	100	31	69	5.70E-03
		EXAFS	3 to 11	16	61	77	21	79	4.60E-01
	soil_initial_I	XANES	-20 to 80	13	88	101	13	87	5.40E-03
		EXAFS	3 to 10	0	99	99	0	100	2.10E-01

Flow: flowering stage. Mat: full maturity stage. I/II/III denote experimental replicates. "a" denotes analytical replicate. Reference compounds used as proxy for Cd-thiol or mixed/ amorph. CdS: Cd-metallothionein, Cd-phytochelatin, Cd-GSH, Cdcysteine and (Cd, Zn, Fe)S. Reference compounds used as proxy for Cd-O: Cd-organic acid complexes, cd phosphate, Cd phytate, and Cd sorbed on goethite and ferrihydrite.

DW Mn Ni Zn Cu period/ growth compartment dry weight (DW) concentration mass concentration mass concentration mass concentration mass stage g µg g⁻¹ μg µg g⁻¹ μg µg g⁻¹ μg µg g-1 μg mean ±sda mean ±sda mean ±sdª mean ±sda mean ±sda mean ±sda mean ±sdª mean ±sda mean ±sdª 1575 239 45.0 3.22 40.5 4.15 109 14.7 9314 796 0.91 0.14 36 6.1 4.0 155 24.1 shoot 0.73 1.35 105 h 14.5 0.61 c 21.8 15.9 h 245 261 h 352 229 b 0 48 016 h 0.69 0 47 с 4 23 0.47 ab 6.49 5.02 h flag leaves maturity 2.81 0.69 b 46.7 2.48 a 132 39.3 а 358 21.3 a 1012 295 а 1.38 0.16 a 3.9 1.14 b 3.54 0.65 b 9.92 2.66 b panicle 4.83 1.01 a 26.9 1.24 b 130 25.6 26.1 5.26 c 125 30 с 1.60 0.35 a 7.75 2.35 а а 4.78 0.69 a 23.0 5.70 a grains vsd = standard deviation of the mean of n = 4 experimental replicates. Letters indicate significant differences of the mean determined using ANDVA (non tranformation: DW, Zn mass; 1/x tranformation: Cu conc.; sqrt transformation: Zn conc., Mi conc., Ni mass; log10 transformation: Mi mass.) The sd was calculated using error progradation as described in equations 4-5.

Table_S 7: Dry weight and micronutrient concentrations in the upper shoot at maturity



Figure_S 1: Overview rice parts analyzed.

At flowering, the roots were separated from the shoots and then the nodes were separated from the shoot. At maturity, roots were separated form the shoot and the shoot was dissected into nodes, straw, and upper shoot. The latter was further dissected into flag leaves, panicle (rachis and spikelets), and grains. For both growth stages, the nodes sampled are defined as 'node I' according to Yamaji and Ma (2014).